

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: YU, GUO-LIANG
EBNER, REINHARD
NI, JIAN
- (ii) TITLE OF INVENTION: NEUTROKINE ALPHA
- (iii) NUMBER OF SEQUENCES: 17
- (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: HUMAN GENOME SCIENCES, INC.
 - (B) STREET: 9410 KEY WEST AVENUE
 - (C) CITY: ROCKVILLE
 - (D) STATE: MD
 - (E) COUNTRY: US
 - (F) ZIP: 20850
- (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Floppy disk
 - (B) COMPUTER: IBM PC compatible
 - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 - (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
- (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER:
 - (B) FILING DATE:
 - (C) CLASSIFICATION:
- (viii) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: BENSON, ROBERT H
 - (B) REGISTRATION NUMBER: 30,446
 - (C) REFERENCE/DOCKET NUMBER: PF343
- (ix) TELECOMMUNICATION INFORMATION:
 - (A) TELEPHONE: (301) 309-8504
 - (B) TELEFAX: (301) 309-8512

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1100 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: DNA (genomic)
- (ix) FEATURE:
 - (A) NAME/KEY: CDS

(B) LOCATION: 147..1001

(ix) FEATURE:

(A) NAME/KEY: sig_peptide

(B) LOCATION: 285..381

(ix) FEATURE:

(A) NAME/KEY: mat_peptide

(B) LOCATION: 147..1001

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

AAATTCAGGA TAACTCTCCT GAGGGGTGAG CCAAGCCCTG CCATGTAGTG CACGCAGGAC	60
ATCAACAAAC ACAGATAACA GGAAATGATC CATTCCCTGT GGTCACCTTAT TCTAAAGGCC	120
CCAACCTTCA AAGTTCAAGT AGTGAT ATG GAT GAC TCC ACA GAA AGG GAG CAG	173
Met Asp Asp Ser Thr Glu Arg Glu Gln	
1 5	
TCA CGC CTT ACT TCT TGC CTT AAG AAA AGA GAA GAA ATG AAA CTG AAG	221
Ser Arg Leu Thr Ser Cys Leu Lys Lys Arg Glu Glu Met Lys Leu Lys	
10 15 20 25	
GAG TGT GTT TCC ATC CTC CCA CGG AAG GAA AGC CCC TCT GTC CGA TCC	269
Glu Cys Val Ser Ile Leu Pro Arg Lys Glu Ser Pro Ser Val Arg Ser	
30 35 40	
TCC AAA GAC GGA AAG CTG CTG GCT GCA ACC TTG CTG CTG GCA CTG CTG	317
Ser Lys Asp Gly Lys Leu Leu Ala Ala Thr Leu Leu Leu Ala Leu Leu	
45 50 55	
TCT TGC TGC CTC ACG GTG GTG TCT TTC TAC CAG GTG GCC GCC CTG CAA	365
Ser Cys Cys Leu Thr Val Val Ser Phe Tyr Gln Val Ala Ala Leu Gln	
60 65 70	
GGG GAC CTG GCC AGC CTC CGG GCA GAG CTG CAG GGC CAC CAC GCG GAG	413
Gly Asp Leu Ala Ser Leu Arg Ala Glu Leu Gln Gly His His Ala Glu	
75 80 85	
AAG CTG CCA GCA GGA GCA GGA GCC CCC AAG GCC GGC CTG GAG GAA GCT	461
Lys Leu Pro Ala Gly Ala Gly Ala Pro Lys Ala Gly Leu Glu Glu Ala	
90 95 100 105	
CCA GCT GTC ACC GCG GGA CTG AAA ATC TTT GAA CCA CCA GCT CCA GGA	509
Pro Ala Val Thr Ala Gly Leu Lys Ile Phe Glu Pro Pro Ala Pro Gly	
110 115 120	
GAA GGC AAC TCC AGT CAG AAC AGC AGA AAT AAG CGT GCC GTT CAG GGT	557
Glu Gly Asn Ser Ser Gln Asn Ser Arg Asn Lys Arg Ala Val Gln Gly	
125 130 135	
CCA GAA GAA ACA GTC ACT CAA GAC TGC TTG CAA CTG ATT GCA GAC AGT	605
Pro Glu Glu Thr Val Thr Gln Asp Cys Leu Gln Leu Ile Ala Asp Ser	

140	145	150	
GAA ACA CCA ACT ATA CAA AAA GGA TCT TAC ACA TTT GTT CCA TGG CTT			653
Glu Thr Pro Thr Ile Gln Lys Gly Ser Tyr Thr Phe Val Pro Trp Leu			
155	160	165	
CTC AGC TTT AAA AGG GGA AGT GCC CTA GAA GAA AAA GAG AAT AAA ATA			701
Leu Ser Phe Lys Arg Gly Ser Ala Leu Glu Glu Lys Glu Asn Lys Ile			
170	175	180	185
TTG GTC AAA GAA ACT GGT TAC TTT TTT ATA TAT GGT CAG GTT TTA TAT			749
Leu Val Lys Glu Thr Gly Tyr Phe Phe Ile Tyr Gly Gln Val Leu Tyr			
	190	195	200
ACT GAT AAG ACC TAC GCC ATG GGA CAT CTA ATT CAG AGG AAG AAG GTC			797
Thr Asp Lys Thr Tyr Ala Met Gly His Leu Ile Gln Arg Lys Lys Val			
	205	210	215
CAT GTC TTT GGG GAT GAA TTG AGT CTG GTG ACT TTG TTT CGA TGT ATT			845
His Val Phe Gly Asp Glu Leu Ser Leu Val Thr Leu Phe Arg Cys Ile			
	220	225	230
CAA AAT ATG CCT GAA ACA CTA CCC AAT AAT TCC TGC TAT TCA GCT GGC			893
Gln Asn Met Pro Glu Thr Leu Pro Asn Asn Ser Cys Tyr Ser Ala Gly			
	235	240	245
ATT GCA AAA CTG GAA GAA GGA GAT GAA CTC CAA CTT GCA ATA CCA AGA			941
Ile Ala Lys Leu Glu Glu Gly Asp Glu Leu Gln Leu Ala Ile Pro Arg			
250	255	260	265
GAA AAT GCA CAA ATA TCA CTG GAT GGA GAT GTC ACA TTT TTT GGT GCA			989
Glu Asn Ala Gln Ile Ser Leu Asp Gly Asp Val Thr Phe Phe Gly Ala			
	270	275	280
TTG AAA CTG CTG TGACCTACTT ACACCATGTC TGTAGCTATT TTCCTCCCTT			1041
Leu Lys Leu Leu			
	285		
TCTCTGTACC TCTAAGAAGA AAGAATCTAA CTGAAAATAC CAAAAAAAAA AAAAAAAAAA			1100

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 285 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met	Asp	Asp	Ser	Thr	Glu	Arg	Glu	Gln	Ser	Arg	Leu	Thr	Ser	Cys	Leu
1					5				10					15	

Lys	Lys	Arg	Glu	Glu	Met	Lys	Leu	Lys	Glu	Cys	Val	Ser	Ile	Leu	Pro	20	25	30
Arg	Lys	Glu	Ser	Pro	Ser	Val	Arg	Ser	Ser	Lys	Asp	Gly	Lys	Leu	Leu	35	40	45
Ala	Ala	Thr	Leu	Leu	Leu	Ala	Leu	Leu	Ser	Cys	Cys	Leu	Thr	Val	Val	50	55	60
Ser	Phe	Tyr	Gln	Val	Ala	Ala	Leu	Gln	Gly	Asp	Leu	Ala	Ser	Leu	Arg	65	70	75
Ala	Glu	Leu	Gln	Gly	His	His	Ala	Glu	Lys	Leu	Pro	Ala	Gly	Ala	Gly	85	90	95
Ala	Pro	Lys	Ala	Gly	Leu	Glu	Glu	Ala	Pro	Ala	Val	Thr	Ala	Gly	Leu	100	105	110
Lys	Ile	Phe	Glu	Pro	Pro	Ala	Pro	Gly	Glu	Gly	Asn	Ser	Ser	Gln	Asn	115	120	125
Ser	Arg	Asn	Lys	Arg	Ala	Val	Gln	Gly	Pro	Glu	Glu	Thr	Val	Thr	Gln	130	135	140
Asp	Cys	Leu	Gln	Leu	Ile	Ala	Asp	Ser	Glu	Thr	Pro	Thr	Ile	Gln	Lys	145	150	155
Gly	Ser	Tyr	Thr	Phe	Val	Pro	Trp	Leu	Leu	Ser	Phe	Lys	Arg	Gly	Ser	165	170	175
Ala	Leu	Glu	Glu	Lys	Glu	Asn	Lys	Ile	Leu	Val	Lys	Glu	Thr	Gly	Tyr	180	185	190
Phe	Phe	Ile	Tyr	Gly	Gln	Val	Leu	Tyr	Thr	Asp	Lys	Thr	Tyr	Ala	Met	195	200	205
Gly	His	Leu	Ile	Gln	Arg	Lys	Lys	Val	His	Val	Phe	Gly	Asp	Glu	Leu	210	215	220
Ser	Leu	Val	Thr	Leu	Phe	Arg	Cys	Ile	Gln	Asn	Met	Pro	Glu	Thr	Leu	225	230	235
Pro	Asn	Asn	Ser	Cys	Tyr	Ser	Ala	Gly	Ile	Ala	Lys	Leu	Glu	Glu	Gly	245	250	255
Asp	Glu	Leu	Gln	Leu	Ala	Ile	Pro	Arg	Glu	Asn	Ala	Gln	Ile	Ser	Leu	260	265	270
Asp	Gly	Asp	Val	Thr	Phe	Phe	Gly	Ala	Leu	Lys	Leu	Leu				275	280	285

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 233 amino acids

(B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

Met	Ser	Thr	Glu	Ser	Met	Ile	Arg	Asp	Val	Glu	Leu	Ala	Glu	Glu	Ala	1	5	10	15
Leu	Pro	Lys	Lys	Thr	Gly	Gly	Pro	Gln	Gly	Ser	Arg	Arg	Cys	Leu	Phe	20	25	30	
Leu	Ser	Leu	Phe	Ser	Phe	Leu	Ile	Val	Ala	Gly	Ala	Thr	Thr	Leu	Phe	35	40	45	
Cys	Leu	Leu	His	Phe	Gly	Val	Ile	Gly	Pro	Gln	Arg	Glu	Glu	Ser	Pro	50	55	60	
Arg	Asp	Leu	Ser	Leu	Ile	Ser	Pro	Leu	Ala	Gln	Ala	Val	Arg	Ser	Ser	65	70	75	80
Ser	Arg	Thr	Pro	Ser	Asp	Lys	Pro	Val	Ala	His	Val	Val	Ala	Asn	Pro	85	90	95	
Gln	Ala	Glu	Gly	Gln	Leu	Gln	Trp	Leu	Asn	Arg	Arg	Ala	Asn	Ala	Leu	100	105	110	
Leu	Ala	Asn	Gly	Val	Glu	Leu	Arg	Asp	Asn	Gln	Leu	Val	Val	Pro	Ser	115	120	125	
Glu	Gly	Leu	Tyr	Leu	Ile	Tyr	Ser	Gln	Val	Leu	Phe	Lys	Gly	Gln	Gly	130	135	140	
Cys	Pro	Ser	Thr	His	Val	Leu	Leu	Thr	His	Thr	Ile	Ser	Arg	Ile	Ala	145	150	155	160
Val	Ser	Tyr	Gln	Thr	Lys	Val	Asn	Leu	Leu	Ser	Ala	Ile	Lys	Ser	Pro	165	170	175	
Cys	Gln	Arg	Glu	Thr	Pro	Glu	Gly	Ala	Glu	Ala	Lys	Pro	Trp	Tyr	Glu	180	185	190	
Pro	Ile	Tyr	Leu	Gly	Gly	Val	Phe	Gln	Leu	Glu	Lys	Gly	Asp	Arg	Leu	195	200	205	
Ser	Ala	Glu	Ile	Asn	Arg	Pro	Asp	Tyr	Leu	Asp	Phe	Ala	Glu	Ser	Gly	210	215	220	
Gln	Val	Tyr	Phe	Gly	Ile	Ile	Ala	Leu								225	230		

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 205 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Met	Thr	Pro	Pro	Glu	Arg	Leu	Phe	Leu	Pro	Arg	Val	Cys	Gly	Thr	Thr		
1				5					10					15			
Leu	His	Leu	Leu	Leu	Leu	Gly	Leu	Leu	Leu	Val	Leu	Leu	Pro	Gly	Ala		
			20				25						30				
Gln	Gly	Leu	Pro	Gly	Val	Gly	Leu	Thr	Pro	Ser	Ala	Ala	Gln	Thr	Ala		
		35					40					45					
Arg	Gln	His	Pro	Lys	Met	His	Leu	Ala	His	Ser	Thr	Leu	Lys	Pro	Ala		
	50					55					60						
Ala	His	Leu	Ile	Gly	Asp	Pro	Ser	Lys	Gln	Asn	Ser	Leu	Leu	Trp	Arg		
65					70					75					80		
Ala	Asn	Thr	Asp	Arg	Ala	Phe	Leu	Gln	Asp	Gly	Phe	Ser	Leu	Ser	Asn		
				85					90					95			
Asn	Ser	Leu	Leu	Val	Pro	Thr	Ser	Gly	Ile	Tyr	Phe	Val	Tyr	Ser	Gln		
			100					105					110				
Val	Val	Phe	Ser	Gly	Lys	Ala	Tyr	Ser	Pro	Lys	Ala	Pro	Ser	Ser	Pro		
		115					120						125				
Leu	Tyr	Leu	Ala	His	Glu	Val	Gln	Leu	Phe	Ser	Ser	Gln	Tyr	Pro	Phe		
	130					135						140					
His	Val	Pro	Leu	Leu	Ser	Ser	Gln	Lys	Met	Val	Tyr	Pro	Gly	Leu	Gln		
145					150					155					160		
Glu	Pro	Trp	Leu	His	Ser	Met	Tyr	His	Gly	Ala	Ala	Phe	Gln	Leu	Thr		
				165					170					175			
Gln	Gly	Asp	Gln	Leu	Ser	Thr	His	Thr	Asp	Gly	Ile	Pro	His	Leu	Val		
			180					185					190				
Leu	Ser	Pro	Ser	Thr	Val	Phe	Phe	Gly	Ala	Phe	Ala	Leu					
		195					200					205					

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 244 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

Met	Gly	Ala	Leu	Gly	Leu	Glu	Gly	Arg	Gly	Gly	Arg	Leu	Gln	Gly	Arg	
1				5					10					15		
Gly	Ser	Leu	Leu	Leu	Ala	Val	Ala	Gly	Ala	Thr	Ser	Leu	Val	Thr	Leu	
			20					25					30			
Leu	Leu	Ala	Val	Pro	Ile	Thr	Val	Leu	Ala	Val	Leu	Ala	Leu	Val	Pro	
		35					40					45				
Gln	Asp	Gln	Gly	Gly	Leu	Val	Thr	Glu	Thr	Ala	Asp	Pro	Gly	Ala	Gln	
	50					55					60					
Ala	Gln	Gln	Gly	Leu	Gly	Phe	Gln	Lys	Leu	Pro	Glu	Glu	Glu	Pro	Glu	
65					70					75					80	
Thr	Asp	Leu	Ser	Pro	Gly	Leu	Pro	Ala	Ala	His	Leu	Ile	Gly	Ala	Pro	
				85					90					95		
Leu	Lys	Gly	Gln	Gly	Leu	Gly	Trp	Glu	Thr	Thr	Lys	Glu	Gln	Ala	Phe	
			100					105					110			
Leu	Thr	Ser	Gly	Thr	Gln	Phe	Ser	Asp	Ala	Glu	Gly	Leu	Ala	Leu	Pro	
		115					120					125				
Gln	Asp	Gly	Leu	Tyr	Tyr	Leu	Tyr	Cys	Leu	Val	Gly	Tyr	Arg	Gly	Arg	
	130					135					140					
Ala	Pro	Pro	Gly	Gly	Gly	Asp	Pro	Gln	Gly	Arg	Ser	Val	Thr	Leu	Arg	
145					150					155					160	
Ser	Ser	Leu	Tyr	Arg	Ala	Gly	Gly	Ala	Tyr	Gly	Pro	Gly	Thr	Pro	Glu	
				165				170						175		
Leu	Leu	Leu	Glu	Gly	Ala	Glu	Thr	Val	Thr	Pro	Val	Leu	Asp	Pro	Ala	
			180					185					190			
Arg	Arg	Gln	Gly	Tyr	Gly	Pro	Leu	Trp	Tyr	Thr	Ser	Val	Gly	Phe	Gly	
		195					200						205			
Gly	Leu	Val	Gln	Leu	Arg	Arg	Gly	Glu	Arg	Val	Tyr	Val	Asn	Ile	Ser	

210		215		220											
His	Pro	Asp	Met	Val	Asp	Phe	Ala	Arg	Gly	Lys	Thr	Phe	Phe	Gly	Ala
225					230					235					240
Val Met Val Gly															

(2) INFORMATION FOR SEQ ID NO:6:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 281 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Met	Gln	Gln	Pro	Phe	Asn	Tyr	Pro	Tyr	Pro	Gln	Ile	Tyr	Trp	Val	Asp
1				5					10					15	
Ser	Ser	Ala	Ser	Ser	Pro	Trp	Ala	Pro	Pro	Gly	Thr	Val	Leu	Pro	Cys
			20					25					30		
Pro	Thr	Ser	Val	Pro	Arg	Arg	Pro	Gly	Gln	Arg	Arg	Pro	Pro	Pro	Pro
			35				40					45			
Pro	Pro	Pro	Pro	Pro	Leu	Pro	Pro	Pro	Pro	Pro	Pro	Pro	Pro	Leu	Pro
			50			55				60					
Pro	Leu	Pro	Leu	Pro	Pro	Leu	Lys	Lys	Arg	Gly	Asn	His	Ser	Thr	Gly
65					70				75						80
Leu	Cys	Leu	Leu	Val	Met	Phe	Phe	Met	Val	Leu	Val	Ala	Leu	Val	Gly
				85					90					95	
Leu	Gly	Leu	Gly	Met	Phe	Gln	Leu	Phe	His	Leu	Gln	Lys	Glu	Leu	Ala
			100					105					110		
Glu	Leu	Arg	Glu	Ser	Thr	Ser	Gln	Met	His	Thr	Ala	Ser	Ser	Leu	Glu
			115				120					125			
Lys	Gln	Ile	Gly	His	Pro	Ser	Pro	Pro	Pro	Glu	Lys	Lys	Glu	Leu	Arg
			130			135					140				
Lys	Val	Ala	His	Leu	Thr	Gly	Lys	Ser	Asn	Ser	Arg	Ser	Met	Pro	Leu
145					150					155					160
Glu	Trp	Glu	Asp	Thr	Tyr	Gly	Ile	Val	Leu	Leu	Ser	Gly	Val	Lys	Tyr
				165					170					175	

Lys	Lys	Gly	Gly	Leu	Val	Ile	Asn	Glu	Thr	Gly	Leu	Tyr	Phe	Val	Tyr			
			180					185					190					
Ser	Lys	Val	Tyr	Phe	Arg	Gly	Gln	Ser	Cys	Asn	Asn	Leu	Pro	Leu	Ser			
		195				200						205						
His	Lys	Val	Tyr	Met	Arg	Asn	Ser	Lys	Tyr	Pro	Gln	Asp	Leu	Val	Met			
	210					215					220							
Met	Glu	Gly	Lys	Met	Met	Ser	Tyr	Cys	Thr	Thr	Gly	Gln	Met	Trp	Ala			
225					230					235					240			
Arg	Ser	Ser	Tyr	Leu	Gly	Ala	Val	Phe	Asn	Leu	Thr	Ser	Ala	Asp	His			
				245					250					255				
Leu	Tyr	Val	Asn	Val	Ser	Glu	Leu	Ser	Leu	Val	Asn	Phe	Glu	Glu	Ser			
			260					265					270					
Gln	Thr	Phe	Phe	Gly	Leu	Tyr	Lys	Leu										
		275					280											

(2) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 338 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

AGGNTAACTC TCCTGAGGGG TGAGCCAAGC CCTGCCATGT AGTGCACGCA GGACATCANC	60
AAACACANNN NNCAGGAAAT AATCCATTCC CTGTGGTCAC TTATTCTAAA GGCCCCAACC	120
TTCAAAGTTC AAGTAGTGAT ATGGATGACT CCACAGAAAG GGAGCAGTCA CGCCTTACTT	180
CTTGCCCTTAA GAAAAGAGAA GAAATGAAAC TGNAAGGAGT GTGTTTCCAT CCTCCCACGG	240
AAGGAAAGCC CCTCTNTCCG ATCCTCCAAA GACGGAAAGC TGCTGGCTGC AACCTTGNTG	300
NTGGCATTGT GTTCTTGCTG NCTCAAGGTG GTGTTNTT	338

(2) INFORMATION FOR SEQ ID NO:8:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 509 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

AATTCGGCAN	AGNAACTGG	TTACTTTTTT	ATATATGGTC	AGGTTTTATA	TACTGATAAG	60
ACCTACGCCA	TGGGACATCT	AGTTCAGAGG	AAGAAGGTCC	ATGTCTTTGG	GGATGAATTG	120
AGTCTGGTGA	CTTTGTTTCG	ATGTATTCAA	AATATGCCTG	AAACACTACC	CAATAATTCC	180
TGCTATTTCAG	CTGGCATTGC	AAAACCTGGNA	GGAAGGAGAT	GAACTCCAAC	TTGCAATACC	240
AGGGGAAAAT	GCACAATTAT	CACTGGGATG	GAGATGTTCA	CATTTTTTTG	GTGCCATTGA	300
AACTGCTGTG	ACCTNCTTAC	ANCANGTGCT	GTTNGCTATT	TTNCCTNCCT	NTTCTNTGGT	360
AACCTCTTAG	GAAGGAAGGA	TTCTTAACTG	GGAAATAACC	CAAAAAAANN	TTAAANGGGT	420
ANGNGNNANA	NGNGGGGNNG	TTNNCNGNN	GNNTTTTNGG	NNTATNTTNT	NNTNGGGNNN	480
NGTAAAAATG	GGGCCNANGG	GGGNTTTTTT				509

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 497 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

AATTCGGCAC	GAGCAAGGCC	GGCCTGGAGG	AAGCTCCAGC	TGTCACCGCG	GGACTGAAAA	60
TCTTTGAACC	ACCAGCTCCA	GGAGAAGGCA	ACTCCAGTCA	GAACAGCAGA	AATAAGCGTG	120
CCGTTTCAGG	TCCAGAAGAA	ACAGTCACTC	AAGACTGCTT	GCAACTGNNT	GCAGACAGTG	180
AAACACCAAC	TATACAAAAA	GGCTCCCTTC	TGNTGCCACA	TTTGGGCCAA	GGAATGGAGA	240
GATTTCTTCG	TCTGGAAACA	TTTTGCCAAA	CTCTTCAGAT	ACTCTTTNCT	CTCTGGGAAT	300
CAAAGGAAAA	TCTCTACTTA	GATTNACACA	TTTGTTCCCA	TGGGTNTCTT	AAGTTTTTAA	360
AGGGGAGTGC	CCTTAGGAGG	AAAAGGGGAT	AAATATTGGC	CAAGGNACTG	GTTANTTTNT	420

AAATATGGTC AGGTTTNTAT ANCTGGTAGG CCTCGCCATG GGCATTNATT CANGGNGAGG 480

NCNNTCTTTT GGGNTGA 497

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 27 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

GTGGGATCCA GCCTCCGGGC AGAGCTG 27

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 33 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

GTGAAGCTTT TATTACAGCA GTTCAATGC ACC 33

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 26 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

GTGTCATGAG CCTCCGGGCA GAGCTG 26

(2) INFORMATION FOR SEQ ID NO:13:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 33 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

GTGAAGCTTT TATTACAGCA GTTCAATGC ACC

33

(2) INFORMATION FOR SEQ ID NO:14:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 28 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

GTGGGATCCC CGGGCAGAGC TGCAGGGC

28

(2) INFORMATION FOR SEQ ID NO:15:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 33 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

GTGGGATCCT TATTACAGCA GTTCAATGC ACC

33

(2) INFORMATION FOR SEQ ID NO:16:

- (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 129 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

GCGGGATCCG CCACCATGAA CTCCTTCTCC ACAAGCGCCT TCGGTCCAGT TGCCTTCTCC	60
CTGGGGCTGC TCCTGGTGTT GCCTGCTGCC TTCCCTGCCC CAGTTGTGAG ACAAGGGGAC	120
CTGGCCAGC	129

(2) INFORMATION FOR SEQ ID NO:17:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 30 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

GTGGGATCCT TACAGCAGTT TCAATGCACC	30
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